AMENDMENTS TO THE SPECIFICATION

Please amend the specification by rewriting the following paragraphs, as set forth below in marked-up form.

In the paragraph beginning on page 1, line 10,

--Among conventional mass-spectroscopic techniques for determining amino acid sequences of peptides are MS/MS analysis using Post-Source Decay technique (PSD) and MS/MS analysis using ESI-Q-TOF mass spectrometry. In PSD analysis, on a MALDI-TOF mass spectrometer, a peptide of interest is ionized and the generated ions (*i.e.*, precursor ions) undergo spontaneous decomposition during flight into different PSD ions, which in turn are separated and detected. In each of these techniques, precursor ions resulting from a peptide are selected and are decomposed on a mass spectrometer into product ions. The resulting peptide fragments are analyzed to provide information on the amino acid sequence of the peptide. In these techniques, however, peptide fragmentation takes place not only in peptide bonds but also in sites other than peptide bonds, resulting in a complex mixture of peptide fragments. This results in mixed spectra of those different fragments, as well as spectra of fragment containing the N-terminus of the peptide of interest and fragment containing the C-terminus of the peptide of interest. Such spectra are generally complicated and difficult to analyze. Though the recent development of search engines such as "Mascot" ~~(http://www.matrixscience.com/)~~ at the web site of Matrix Science (www.matrixscience.com) has enabled database searches to determine the peptide sequence from such complicated spectrum patterns, the number of identifiable peptides has been limited since reference can be made only to the peptides available on these databases.--

In the paragraph beginning on page 2, line 22,

--Relying on chemical modification, however, this approach has disadvantages that the efficiency of the decomposition into product ions is limited, that the selectivity of the cleavage site is

insufficient, and that the efficiency of the decomposition into ~~prooduct~~ product ions, as well as the selectivity of the cleavage sites, can vary significantly depending on the internal sequences of the peptide, limiting the number of identifiable peptides.--

In the paragraph beginning on page 13, line 20,

--Fig. 1 shows the PSD spectra of laminin pentapeptide that is coupled to ~~N-eiotinylcysteic acid~~ N-biotinylcysteic acid. Fig. 2 shows the PSD spectra of laminin pentapeptide that is not coupled to N-biotinylcysteic acid. In each figure, horizontal axis indicates the mass-to-charge ratio of the ions (m/z), whereas vertical axis indicates the relative intensity of the ions (Int.). A single alphabet letter followed by a parenthesized number shown above each peak of the decay products indicates the position of cleaved peptide bonds. The letter y signifies that the peptide is derived from the C-terminus and each number indicates the number of remaining amino acid residues.--